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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=5; day=27; hr=13; min=35; sec=56; ms=931;]

=====

Reviewer Comments:

SEQUENCE LISTING

<110> Nordheim et al.

<120> Method For Detecting Biomolecules

Please insert the following mandatory numeric identifiers and their responses below the <120> line:

<130> this represents the file reference number: the response is usually the attorney docket number

<140> US 10/527,055 (this is the current application number)

<141> 2005-05-18 (this is the current application filing date)

<210> 1

<211> 9

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 1

AVFPSIVGR

Several errors above: 1) the "<212> PROTEIN" line is invalid: per the Sequence Rules, use PRT to denote an amino acid sequence; 2) Please show "UNKNOWN" as "Unknown" (only the initial letter is in upper-case); 3) Please insert a mandatory "<220>" above the <223> line; <220> is mandatory whenever <221>, <222>, or <223> is shown. It is a "header" only: it never has a response; 4) although the <213> response is "Unknown", in the <223> response, please try to furnish more information regarding the source of the genetic material; also, you do not need to

indicate Figures; 5) do not use one-letter amino acids. Per the Sequence Rules, use three-letter amino acids, with one space between each amino acid. Please number the amino acids under every 5 amino acids, starting with "1"; do not use TAB codes between amino acid numbers: TABs cause misaligned numbers when processed: use space characters, instead. Please show a maximum number of 16 amino acids per line.

```
<210> 10
<211> 13
<212> PROTEIN
<213> UNKNOWN
<223> Fig. 4A - Spot 4 - Enolase 1, alpha non neuron
<400> 10
YITPDQLADLYK
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Besides all of the errors listed in the first paragraph above, there is a discrepancy in this sequence: although the <211> response is "13", only 12 amino acids are shown. Please ensure, in subsequent sequences, that the <211> response matches the actual number of amino acids in the sequence.

Application No: 10527055

Version No: 1.0

Input Set:**Output Set:**

Started: 2010-05-27 10:29:07.908
Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (1)
W 112	Upper case found in data; Found at position(0) SEQID(1)
W 112	Upper case found in data; Found at position(1) SEQID(1)
W 112	Upper case found in data; Found at position(2) SEQID(1)
W 112	Upper case found in data; Found at position(3) SEQID(1)
W 112	Upper case found in data; Found at position(4) SEQID(1)
W 112	Upper case found in data; Found at position(5) SEQID(1)
W 112	Upper case found in data; Found at position(6) SEQID(1)
W 112	Upper case found in data; Found at position(7) SEQID(1)
W 112	Upper case found in data; Found at position(8) SEQID(1)
E 310	Invalid sequence type in <212> in SEQID: (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 112	Upper case found in data; Found at position(1) SEQID(2)
W 112	Upper case found in data; Found at position(2) SEQID(2)
W 112	Upper case found in data; Found at position(3) SEQID(2)

Input Set:

Output Set:

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Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
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Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

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W 112	Upper case found in data; Found at position(5) SEQID(2)
W 112	Upper case found in data; Found at position(6) SEQID(2)
W 112	Upper case found in data; Found at position(7) SEQID(2)
W 112	Upper case found in data; Found at position(8) SEQID(2)
W 112	Upper case found in data; Found at position(9) SEQID(2)
E 310	Invalid sequence type in <212> in SEQID: (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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E 310	Invalid sequence type in <212> in SEQID: (4)
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Input Set:

Output Set:

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Total Errors: 306
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Actual SeqID Count: 153

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Input Set:

Output Set:

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Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
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Input Set:

Output Set:

Started: 2010-05-27 10:29:07.908
Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
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Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

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W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Nordheim et al.

<120> Method For Detecting Biomolecules

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<211> 9

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

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AVFPSIVGR

<210> 2

<211> 10

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 2

GYSFTTAER

<210> 3

<211> 16

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SYELPDGQVITIGNER

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<211> 18

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<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

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<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70

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<210> 6

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<211> 23

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<213> UNKNOWN

<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70
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<211> 13

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CEFQDAYVLLSEK

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AAVEEGIVLGGGCALLR

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ISSVQSIVPALEIANHR

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<400> 30
EALLSSAVDHGSDEAR

<210> 31
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AAVPSGASTGIYEALRLR

<210> 32
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<400> 32
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<400> 35
FAAATGATPIAGR

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 <212> PROTEIN
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 FIPGIFTNQLQAAR

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SYELPDGQVITIGNER

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VVTV

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AAVPSGASTGIYEALRL

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ETIA

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VLATAFD

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ETIA

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DSFNITFFSETGAGK

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ETIDLVLR

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AVFVDLEPTVIDEVR

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YQPPTVVP

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DSFNITFFSETGAGK

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EIADGLCLEV

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QSIVPALEIA

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CEFQDAYVLLSEK

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EEGIVLGGGCALLR

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SIVPALEIA

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VQQTIVQDL

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VILVG

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VVTVPAYF

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TGIP

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GYSFTTT

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PVLLTEAPLNPK

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SYELPDGQVITIGNER

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PVLLTEAPLNPKE

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VVTV

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DAGTIAGLNVLR

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VVTV

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GHPTEVDLY

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AVFVDLEPTVIDEVR

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EIIDLVLDR

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EGIVLGG

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